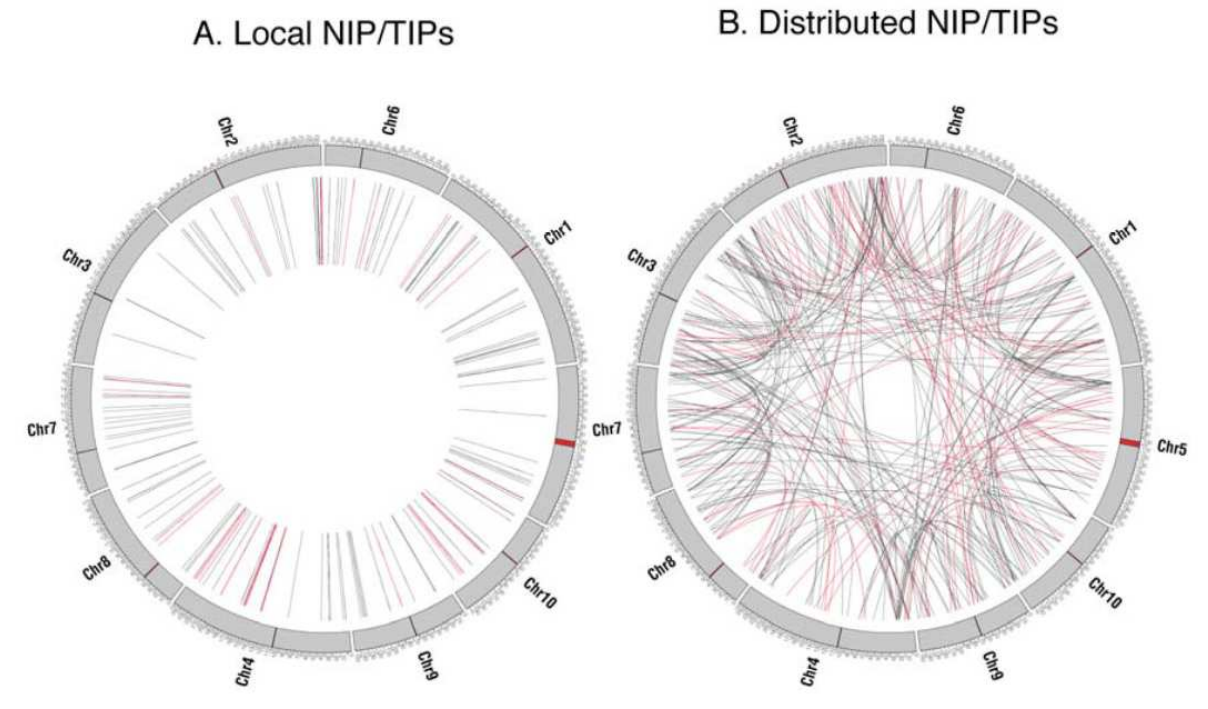


APPENDIX A. Nearly identical paralogs in maize genome

Modified from a paper published in *Science* 2009, 326: doi:1126/ science.1178534

Nearly identical paralogs (NIPs) are genes with pairwise alignments of ≥ 500 bp, $\geq 98\%$ identity, and $\geq 95\%$ coverage with other genes (Emrich et al, 2007). Of maize-filtered genes, 2.5% (828 out of 32,540) were NIPs from 386 families, most of which have only two members ($n = 349$); the largest has nine members. Almost half (46%) of the NIP pairs had both members physically linked within 200 kb of each other, whereas in most of the remaining cases, the two members were distant from each other or on different chromosomes (fig. S18).

Figure S18. Distribution of NIP/TIP pairs. 222 NIPs exhibit 100% identity; these TIPs (Totally Identical Paralogs) are highlighted in red. (A) Local NIP/ TIP pairs are located within 200 kb of each other; (B) Distributed NIP pairs are >200 kb apart or on different chromosomes. It has been hypothesized that different mechanisms are responsible for the origins of these two classes of NIPs (S63). Although NIPs are distributed across the genome, some regions (e.g., 2L and 4S) have elevated rates of inter-chromosomal NIPs. These do not, however, reflect known segment duplication events, arguing against paralog homogenization as a mechanism for the origin of NIPs. On the basis of array-CGH experiments $\sim 5\%$ of NIPs have stronger signals in B73 than Mo17 genomic DNA (S64), suggesting that Mo17 may have only a single copy of what in the B73 genome are NIP pairs. Centromere positions are from (S44).



REFERENCE

Emrich, S. J., Li, L., Wen, T.-J., Yandeu-Nelson, M. D., Fu, Y., Guo, L., Chou, H.-H., et al. (2007). Nearly identical paralogs: implications for maize (*Zea mays* L.) genome evolution. *Genetics*, 175(1), 429–39. doi:10.1534/genetics.106.064006